Mathematical Modeling and Epidemic Prediction of COVID-19 of the State of São Paulo, Brazil

Pedro Alexandre da Cruz, Leandra Cristina Crema Cruz

Collegiate Exact and Biotechnological Sciences of the Federal University of Tocantins – UFT, Brazil

Abstract—*The Coronavirus pandemic, COVID-19, has taken the lives of several thousand people worldwide, causing many regions and countries to order the closure of their borders, with yet unpredictable global consequences. This pandemic represents a global public health emergency that has never been seen in recent times. In this work, we conducted an investigation of the current coronavirus outbreak (COVID-19) in the State of São Paulo, Brazil, from a mathematical modeling perspective. We seek to describe the different paths of dynamic transmission of infection, the size of the epidemic in the State of São Paulo and to emphasize the role of strict isolation policy in the transmission and dissemination of COVID-19. This research is based on a new mathematical model that is an extension of the SEIR family of compartmental models. As a result of the computational simulations, we show how the social measures of isolation, quarantine and treatment/monitoring of the infected individuals can influence the model parameters and change the cases rates of infected individuals and individuals exposed over time. The predictive capacity of this model, like most mathematical models, is limited by the accuracy of the available data. Problems regarding the accuracy, standard and reliability of the available data are beyond the scope of this work.*

Keywords—*Coronavirus, COVID-19, Epidemic Prediction,Mathematical Modeling, São Paulo.*

I. INTRODUCTION

On December 31, 2019, the World Health Organization (WHO) had been alerted by Chinese authorities that the Chinese city of Wuhan, Hubei province, recorded an outbreak of respiratory disease. The new Coronavirus was identified as the causative agent of this disease and was isolated from a single patient in early January 2020 and later found in 16 more patients [1,2]. Coronavirus cases were exported to other Chinese cities and also exported internationally, which triggered a global outbreak of the new Coronavirus. This new virus is believed to have originated at the Huanan Seafood Market, a wholesale market for live animals and seafood in Wuhan, considered the main source of this epidemic, as it was found that 55% of the first 425 confirmed cases were linked to the market [2]. But there is uncertainty about several aspects of the Covid-19 origin story that scientists are trying hard to unravel, including which species passed it to a human. It appears that this is the third zoonotic human Coronavirus emerging in this century. In the years 2002/2003 the SARS-CoV pandemic hit China and spread to 37 countries, and in 2012 the MERS-CoV emerged, which spread to 37

countries and reached 4 continents. The symptoms of COVID-19 include fever, fatigue, difficulty breathing, dry cough and in the most severe cases, pulmonary infiltration. These symptoms are similar to the symptoms caused by infections by SARS-CoV and MERS-CoV [3].

The National Health Commission of China has developed a system to facilitate the identification and classification of patients. To reduce the spread of the virus, the Chinese government has progressively implemented the Wuhan metropolitan quarantine and several nearby cities since 23 January 2020. Countless airports and train stations domestic, in addition to international airports, have adopted temperature screening measures to detect individuals with fever. On February 10, 2020, more than 42,600 people in China were diagnosed with Coronavirus [4] and the World Health Organization (WHO) formally declared the outbreak of the new Coronavirus a Global Public Health Emergency of International Interest.

In Brazil, the first case of the new Coronavirus was confirmed on February 26, 2020. It was a man, from the State of São Paulo, 61 years old, who was in Italy between February 9 and 21, 2020, period with a significant increase

in the number of cases in that country [5]. On February 5, an urgent measure, Brazilians were repatriated and to leave Wuhan, the epicenter of the pandemic, China. On April 17, more than 12,000 people in the State of São Paulo were diagnosed with Coronavirus [6]. On March 24, 2020, the São Paulo government decreed quarantine across the state, ordering the closure of all non-essential trade and services. However, in order to function, the quarantine requires the adherence of state citizens to personal protection and public health interventions, including a reduction of effective contacts in transmission, separation and restriction during quarantine.

What is known so far is that the dynamics of the COVID-19 infection is affected by several factors that add major challenges to the control of the disease, for example, the incubation period of the disease that varies from 2 to 14 days, and during throughout this period, infected individuals may have no symptoms, but are able to transmit the disease to other individuals [7]. Coronavirus is a new virus and there are no antiviral drugs or vaccines available, so the control of this disease is related to the immediate detection and isolation of symptomatic cases. From the point of view of health management, the dynamics of infection of the disease and the prediction of its spread over time is of great importance in saving lives and minimizing the social and economic consequences of this disease. In the scientific community, this problem has been studied by several communities, such as the modeling of biological systems [12] and epidemiological mathematics [9].

Some studies on mathematical modeling have already been performed to describe and understand the COVID-19 pandemic.

Most of the models used in these works have significantly emphasized the human-to-human direct transmission pathway, as is the case of the work by Wu et. al. [8]. In this work they introduced the susceptible - exposed - infected - recovered (SEIR) model to describe the dynamic transmission of the disease, and provided an estimate of the size of the epidemic in Wuhan in addition to predicting the extent of the epidemic's risks to domestic public health and global. Wu et. al. [8] also estimated that the basic reproductive number for COVID-19 was around 2,68. Sameni [10] proposed a study based on a mathematical model that is an extensions of the SEIR family of compartmental models, and showed how social measures of isolation and quarantine can alter mortality rates and the number of cases of infected individuals over time. Tang et. al. [11] suggested a deterministic model incorporating the clinical condition of the disease and intervention measures, and found that the reproductive

number could be up to 6,47 and that intervention strategies such as intensive contact tracking followed by quarantine and isolation, can effectively reduce reproductive control and the risk of transmission. A computational modeling of possible epidemic trajectories to estimate the size of the disease outbreak in Wuhan was performed by Imai et. al. [13]. All of these models do not take into account the role of the environment in the transmission of COVID-19, for example, when infected individuals cough, these individuals can spread the virus to the environment through droplets, infecting others who have had contact with same areas. There is still a probability that the virus will survive in the environment for several days, for example, the Coronavirus can survive on inanimate surfaces with plastic or glass for up to 9 days [14], increasing the risk of contamination to the individual when in contact with these types of surfaces [15].

Yang and Wang [16] presented a new mathematical model to investigate the outbreak of COVID-19 in Wuhan, and this new model describes the various routes of transmission in the dynamics of the disease and also emphasizes the environmental assignment in the transmission and spread of the disease. This model has a set of differential equations that in addition to considering susceptible, exposed, infected and recovered individuals, it also has an equation that represents the environmental reservoir, that is, it considers that a susceptible individual can acquire COVID-19 through interaction with the contaminated environment, with an infectious but asymptomatic individual, or with an infectious and symptomatic individual.

In present work, we used the SEIR-A mathematical model proposed by Yang and Wang [16] to carry out the mathematical modeling of the COVID-19 Epidemic in the State of São Paulo, Brazil. This model was applied for an epidemic period from March 24, 2020 to April 24, 2020 and also provides a prognosis of the spread of COVID-19 for the next 250 days in the State of São Paulo. This new model incorporates three transmission routes such as the environment-to-human and human-to-human routes, and in particular, a new differential equation is introduced that represents the concentration of Coronavirus in the environmental reservoir. Several works in mathematical modeling have used constant transmission rates to describe and understand the COVID-19 pandemic. In our work, transmission rates depend on environmental conditions and epidemiology that change over time. For example, when the level of infection is very high, we consider that individuals take necessary measures to reduce contact with infected individuals and with the environment that is contaminated, aiming at the protection of your family and

your own protection. These measures lead to a reduction in the average rates of disease transmission. In order to obtain the numerical results, strict control measures were considered, such as quarantine and isolation to reduce contact between individuals, and all these factors are taken as varied transmission rates. Furthermore, in the present work, numerical tests were performed using constant transmission rates to compare the results with variable rates. When compared, the results obtained with constant rates showed an extremely high number of infected individuals and notoriously unrealistic, generating misleading information about infection with the Coronavirus.

II. MATHEMATICAL MODELING

For the mathematical formulation of this model, the total human population was initially divided into four classes:

- *1st class:* susceptible individuals (*S*), individuals who have not yet acquired the disease;

- *2nd class:* exposed individuals (*E*), individuals who are in the incubation period. They have no symptoms, but

are capable of infecting other individuals;

- *3rd class:* infected individuals (*I*), individuals of the infected class and have completely developed

where Δ represents the population inflow and A is the concentration of the Coronavirus in the environment. The parameter m_D represents the mortality rate induced by the disease, μ is the natural mortality rate of human hosts, γ is the recovery rate from COVID-19 infection and α^{-1} is the incubation period between infection and the onset of disease symptoms. The parameters θ_1 and θ_2 are, respectively, the rates of exposed and infected individuals that contribute to the Coronavirus environmental reservoir and σ is the removal rate of the virus from the environment. The functions $T_E(E)$ and $T_I(I)$ represent human-to-human transmission rates between exposed and susceptibleindividuals, and between infected and susceptible individuals, respectively, and in this work are given by:

$$T_E(E) = \frac{T_{E0}}{1+cE} \quad \text{and} \quad T_I(I) = \frac{T_{I0}}{1+cI} \quad (2)$$

WhereT_{E0} andT_{I0} express the maximum values of transmission rates. The function$T_A(A)$ represents the environmental-to-human transmission rate and is given by:

$$T_A(A) = \frac{T_{A0}}{1+cA} \quad (3)$$

symptoms of the disease and are capable of infecting other individuals;

- *4th class:* recovered individuals (*R*), who are the cured individuals and/or individuals who died.

Therefore, with this mathematical formulation, classes$E$ and I of the model contain asymptomatic infected individuals and symptomatic infected individuals, respectively.InSIR models, asymptomatic infected individuals (class E) are not considered.

The mathematical model used in this work to describe the transmission dynamics of the COVID-19 pandemic in the State of São Paulo is given by the following system of ordinary differential equations:

$$\frac{dS}{dt} = \Delta - T_E(E)SE - T_I(I)SI - T_A(A)SA - \mu S,$$

$$\frac{dE}{dt} = T_E(E)SE + T_I(I)SI + T_A(A)SA - (\alpha + \mu)S,$$

$$\frac{dI}{dt} = \alpha E - (m_D + \gamma + \mu)I, \quad (1)$$

$$\frac{dR}{dt} = \gamma I - \mu R,$$

$$\frac{dA}{dt} = \theta_1 E + \theta_2 I - \sigma A,$$

where T_{A0} it expresses the maximum value of this rate andthe constant *c* is an adjustment coefficient to the transmission rates

Specifically, in this work we made the following assumptions:

- $T_E(E)$, $T_I(I)$ and $T_A(A)$ are positive functions;

- The variables that make up infections in this model are the exposed (*E*), infected (*I*) and theconcentration of Coronavirus in the environment (*A*). According to Yang and Wang [16] the infection matrix *M* and the transition matrix *U* are given by:

$$M = \begin{bmatrix} T_E(0)S_0 & T_I(0)S_0 & T_A(0)S_0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \text{and} M = \begin{bmatrix} \alpha + \mu & 0 & 0 \\ -\alpha & w_1 & 0 \\ -\theta_1 & -\theta_2 & \sigma \end{bmatrix} \quad (4)$$

Where $w_1 = m_D + \gamma + \mu$. The basic reproduction number $\Re_0$ is defined as the number of secondary infections that an infected individual is able to create during his period of infection, since the other individuals are susceptible. In the model used in this work, the basic reproduction number $\Re_0$ is defined as the spectral radius of the matrix MU^{-1} (see [17]), thus obtaining,

$$\Re_0 = \rho(MU^{-1}) = \frac{T_E(0)S_0}{\alpha+\mu} + \frac{\alpha T_I(0)S_0}{W_1(\alpha+\mu)} + \frac{(W_1\theta_1 + \alpha\theta_2)T_A(0)S_0}{\sigma W_1(\alpha+\mu)} = \Re_1 + \Re_2 + \Re_3 \qquad (5)$$

and this number provides us with a quantification of the risk of the disease. $\Re_0 = 1$ it is a threshold below which the generation of secondary cases is insufficient to maintain infection in the human community. If $\Re_0 < 1$ the number of infected individuals tends to decrease and the disease tends to disappear, however if $\Re_0 > 1$ the numbers of infected individuals tends to increase, and the disease tends to persist. The first terms $\Re_1$ and $\Re_2$ measure the contributions of human-to-human transmission routes. The term $\Re_1$ measures the contribution of transmission from individuals exposed to susceptible individuals, while $\Re_2$ measures the contribution of transmission from infected individuals to susceptible individuals. The third term of equation (5), $\Re_3$, represents the contribution of the environmental-to-human transmission route. These three modes of transmission jointly model the overall risk of infection by the COVID-19 outbreak.

III. NUMERICAL RESULTS

The results were obtained from the numerical simulations performed with the mathematical model proposed by the system of equations (1). For numerical validation and computational simulations of the model, we used data from the epidemic in the State of São Paulo, published daily by newspapers and other sources [5,6], data daily reporting new cases of COVID-19, cumulative cases and deaths caused in the State of São Paulo, Brazil.

The model was implemented in the mathematical software SCILAB and we performed numerical simulations for an epidemic period starting on March 24, 2020 until April 24, 2020. The estimated population for the State of São Paulo is over 45 million habitants and the State was placed quarantine on March 24, 2020, by the current governor. The preventive measure requires the closure of trade and maintains only essential services, such as health, food and security. In our simulations we will consider that only a relatively "small" number of people have traveled to the State of São Paulo since the beginning of the quarantine, and thus the inflow rate (Δ) of the model is based only on the number of newborns in the state. The average recovery period is approximately 15 days according to [18], and so we define the recovery rate from the disease as $\gamma = 1/15$ per day. The values of transmission rates T_{E0} and T_{I0} can be found in a recent work by Tang et. al. [11]. Some members of the Coronavirus family can survive in the environment since a few hours to several days [14], and we assume the value of 1 day in our work, that is, the virus removal rate is daily ($\sigma = 1$). The incubation period of the infection varies between 2 and 14 days, with average values of 5 to 7 days [18], and so we assume $\alpha^{-1} = 1/7$. As we know, the state government has implemented a strict isolation policy and medical care has been offered to confirmed cases, so the chance of infected individuals spreading the Coronavirus to the environment can be considered low, and in this way, we consider in this paper that $\theta_2 = 0$ and $\theta_1 > 0$ it is so $W_1\theta_1 > 0$. These and other remaining parameters, their values and respective sources are given in Table 1.

Table 1: Definition and values of parameters used in computational modeling.

Parameters	Definition of parameters	Estimated mean value	Source
T_{E0}	Transmission constant between *S* and *E*	6.02×10^{-9}/person/day	[11]
T_{I0}	Transmission constant between *S* and *I*	1.22×10^{-9}/person/day	[11]
T_{A0}	Transmission constant between *S* and *A*	fitting by data	–
c	Transmission adjustment coefficient	fitting by data	–
θ_1	Virus shedding rate by exposed people	fitting by data	–
θ_2	Virus shedding rate by infected people	0 per person per day	–

Δ	Influx rate	1659.26	[21,22,23]
m_D	Disease-induced death rate	0.0372 per day	[24,26]
μ	Average natural death rate	$3.5x10^{-5}$ per day	[27]
$α^{-1}$	Averageincubationperiod	7 days	[18]
γ	Recovery rate fromdisease	1/15 per day	[18]
σ	Removal rate of virus from the environment	1 per day	[20]

However, three other parameters need to be determined: the adjustment coefficient (c), the rate($θ_1$) and the environment-to-human transmission constant (T_{A0}). Emphasizing that most of the published works do not take into account the environmental composition for infection by COVID-19 and, therefore, the value of these three parameters are not available in the literature. In addition, most of these studies consider transmission rates constant over time in their simulations. In the present work, the values of these three parameters are estimated similarly as done in [19], so that the model was adjusted to the cases of COVID-19 infection reported daily to the State of São Paulo from March 24 to April 24, 2020 using the least squares method. The initial conditions (Ci) for our system of ordinary differential equations is defined as:Ci = (S(0), E(0), I(0), R(0), A(0)) = (45919049, 800, 810, 10, 10000), according to data reported in the media daily.

Figure 1 shows the number of cumulative confirmed cases in the period from March 24 to April 24, 2020 in the State of São Paulo versus the adjustment curve obtained by adjusting data using the least squares method. The values of the parameters and their respective confidence intervals are shown in Table 2. The mean square error obtained for the adjustment of the data was 0.00831.

Table 2: Estimated parameters obtained by data fitting.

Parameters	Fittingvalue	ConfidenceInterval
T_{A0}	$6.39x10^{-10}$	$(0,1.086x10^{-9})$
c	$7.48x10^{-5}$	$(3.793x10^{-5},9.351x10^{-5}$
$θ_1$	4.026	(1.225, 24.322)

We can see in Figure 1 that the SEIR-A model based on the dynamic propagation of COVID-19 has a good agreement between the numerical solution obtained via mathematical modeling with the real data for the number of confirmed cases. In addition, the adjustment curve for the

number of confirmed cases is quite consistent with the reported data.

We also used the SEIR-A model to predict the spread of COVID-19 in the State of São Paulo, for the next 250 days. Using computational mathematical modeling, we obtain the trend for the development of the number of cumulative cases of infected individuals (*I*) and for exposed individuals (*E*), as shown in Figure 2. For this numerical simulation, we use the transmission rates given in the equations (2) and (3), the parameters of Table 1 and the results of data adjustment presented in Table 2.

Based on the results presented in Figure 2, we believe that the infection levelwould continueincreasing approximately for about 70 to 80 days from March 24, 2020, marked as day zero / initial day in our simulation, and the cumulative number of confirmed cases by the Coronavirus in the State of São Paulo reach a peak value around 39,000 infected individuals at June 2, 2020.
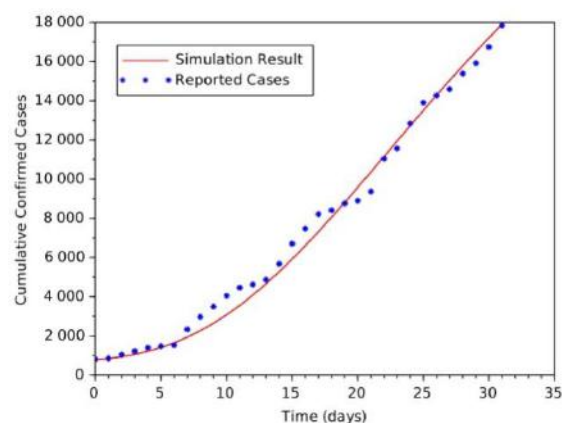

Fig. 1: Cumulative confirmed cases in the period from March 24, 2020 to April 24, 2020 for the State of São Paulo, Brazil. Note: Solid line, in red, denotes the result of the computer simulation and the asterisks, in blue, denote the reported cases of COVID-19.
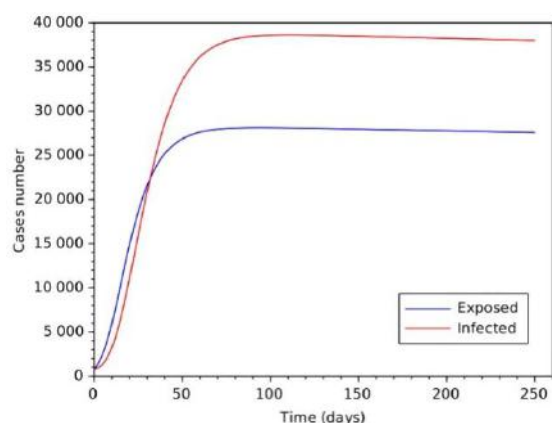
Fig. 2: Results of the numerical simulation to predict the cumulative number cases of Coronavirus in the State of São Paulo, Brazil.

Therefore, after the cumulative number of confirmed cases reaches 39,000 infected individuals on June 2, 2020, new cases may not appear, provide that a strict policy of social isolation continues to be implemented and followed in the State of São Paulo. To better understanding of the spread of COVID-19 in the State of São Paulo, the transmission rates of the new Coronavirus was analyzed. We can see in equations (2) and (3) that transmission rates are related to the number of exposed individuals (E), infected (I) and the concentration of new Coronavirus in the environment (A) that change according to the time. From there, the transmission rate trends for the State of São Paulo over time were obtained, as shown in Figure 3. It can be seen that the transmission rates of the Coronavirus continue to decrease among susceptible-exposed individuals (S-E), susceptible-infected (S-I) and between susceptible-environment (S-A).
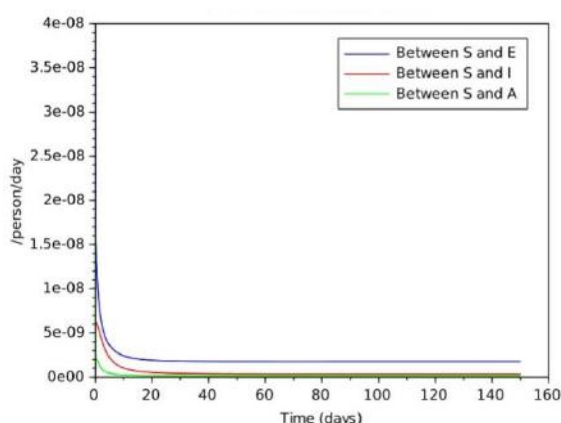

Fig. 3: Behavior of Coronavirus transmission rates in the State of São Paulo, Brazil.

We believe that this fact may indicate that the emergency intervention and isolation measures imposed by the government of the State of São Paulo and also medical resources offered in the affected areas in the initial stage of the transmission of COVID-19 played a crucial role in reducing the spread of the disease epidemic.

Using equation (5), the parameter values given in Table 1 and the adjusted parameter values presented in Table 2, the basic reproduction number ($\Re_0$) was obtained. Specifically, we find the following values:

$$\Re_1 = 1.9344, \Re_2 = 0.3113 \text{ and } \Re_3 = 0.8288$$

Thus obtaining the basic reproduction number$\Re_0 = 3.0745$. In this case, as$\Re_0 > 1$, the numbers of infected individuals tend to increase and the disease tends to persist in the State of São Paulo, Brazil. Among the three components, the greatest value$\Re_1$ comes from the transmission of exposed individuals to susceptible individuals since the exposure of these individuals has no symptoms and they can easily spread the infection to other people when in contact. The component$\Re_2$ comes from transmitting infected individualsto susceptible individuals. It is observed that$\Re_2$ it is the least valuable component, probably due to the strict policy of isolation of infected symptomatic individuals imposed by the state governor. The component$\Re_3$ represents the contribution of the environmental – human route, and it can be seen that this component is making a significant contribution to the overall risk of infection in the State of São Paulo, Brazil.

3.1. Variation study of theθ_2 parameter

In the SEIR-A model, the$\theta_2$parameter represents the rateof infected individuals that contribute to the Coronavirus environmental reservoir. As is well known, the State of São Paulo was placed in social isolation from March 24, 2020, determining the closure of all trade and non-essential services. To function, the social isolation requires the adherence of citizens of the State to personal protection and public health interventions, including a reduction of effective contacts in transmission, separation and restriction during social isolation. With a strict isolation policy and medical care being offered to confirmed cases, the chance of infected individuals contributing to the Coronavirus environmental reservoir can be considered low, that is,$\theta_2 = 0$. The results obtained with the numerical simulation computational for different values of the parameterθ_2 are presented in Table 3 and Figure 4. Table 3 presents numerical results obtained for different values of the parameter$\theta_2$for some specific dates that were compared with real data from cases confirmed by COVID-19. Figure 4 shows the simulation of the parameter$\theta_2$for the period under study (March 24 to April 24, 2020), comparing the decrease in the isolation policy

with the increase in confirmed cases of infected individuals   in   the   State   of   São   Paulo,   Brazil.

Table 3: Predictions of the confirmed cases for differents values of θ_2 parameter.

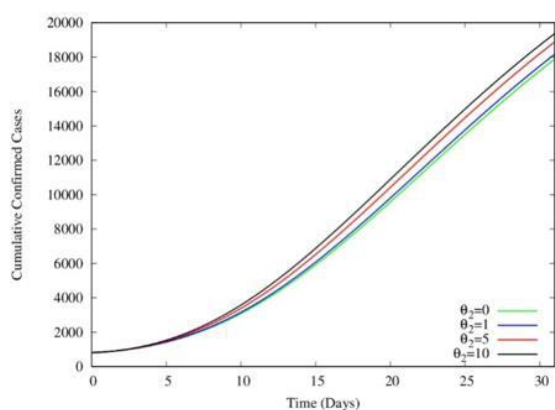| Date	25/03	30/03	05/04	11/04	16/04	20/04	24/04
Predictedconfrimed cases$\theta_2 = 0$	860	1657	4661	8057	11132	14276	17840
Predictedconfrimed cases$\theta_2 = 1$	860	1680	4781	8251	11391	14541	18265
Predictedconfrimed cases$\theta_2 = 5$	862	1757	5142	8813	12057	15255	18890
Predictedconfrimed cases$\theta_2 = 10$	863	1827	5437	9245	12550	15765	19366
Real data of confirmed cases	862	1537	4620	8216	11043	14267	17826

Fig. 4: Effects of the policy of social isolation and medical care for confirmed cases of infected people in the State of São Paulo, Brazil, between March 24 and April 24, 2020.

When comparing the results obtained in the numerical simulations with the real data from confirmed cases, it is clear that the mathematical modeling makes a very satisfactory prediction of the cases that occurred in the period from March 24 to April 24, 2020, as shown in Table 3. In particular, the predictions on April 20 and 24, 2020 are 14276 and 17840 cases, respectively, values very close to the actual number of confirmed cases of 14267 and 17826.

It is verified for the parameter $\theta_2 > 2$ that the duration and reduction appropriate social isolation interferes with

the number of infected individuals. For example, for $\theta_2 = 1$ the predicted cases are 18265 on April 24, 2020, a slightly distant value from the current number of confirmed cases of 17826, with a difference of 439 infected individuals. When the value of θ_2 even more is increased, that is, when there is a shorter social isolation duration, we can observe a discrepancy between the predicted cases and the real

confirmed cases. For example, for $\theta_2 = 10$, the predicted cases are 19366 infected individuals while the real confirmed cases are 17826. Therefore, according to our mathematical modeling it is clear that the appropriate duration of social isolation has significantly decreased the number of infected individuals in the State of São Paulo, Brazil.

3.2. Variation study of the σ parameter

Finally, an analysis is made of the removal rate of Coronavirus from the environment using the SEIR-A model. Figure 5 shows the change in the number of confirmed cases of infected individuals in the State of São Paulo. In this figure we compare the increase in the removal rate of Coronavirus from the environment with the decrease in confirmed cases of infected individuals.
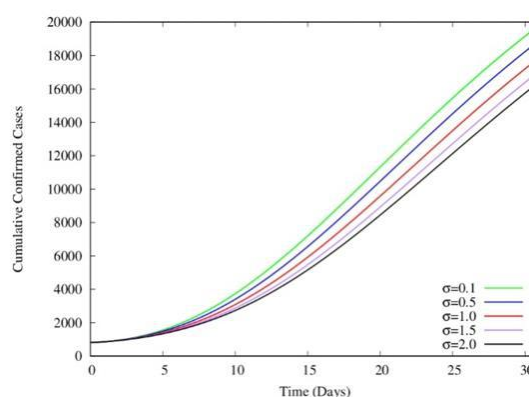

Fig. 5:Effects of the removal rate of Coronavirus from the environment in the State of São Paulo for confirmed cases of infected people.

The change in the removal rate of Coronavirus from the environment changes the number of confirmed cases of infected individuals (Figure 5). For example, when the removal rate of Coronavirus from the environment is 10% ($\sigma = 0.1$),predicted cases are 19823 infected individuals on April 24,2020, while the real number of cases confirmed are 17826. We can observe a discrepancy between the predicted cases and the real confirmed cases, with a difference of 1997 infected individuals. When the removal rate is 100% ($\sigma = 1$), in this case the Coronavirus survival rate is around 24 hours according to [19], and the predicted cases are 17840 infected individuals, a number very close to the actual number of confirmed cases. Therefore, it is observed that when the removal rate of Coronavirus from the environment increased from 10% to 100%, the predict cumulative number of infected individuals decreased in 1983 individuals. According to the results of this numerical simulation, we believe that more Coronavirus tests should be carried out and in this way the sources of infection could be dealt with more quickly. Subsequently, in addition to treating individuals with positive diagnoses, perform continuous tracking of new cases, placing them in strict isolation, thus reducing contact with the environment and thus increasing the rate of removal of the Coronavirus.

The results presented in Figure 6, are equivalent to a numerical test that was performed using constant transmission rates in numerical simulations, that is, $c = 0$ was taken in equations (2) and (3). Therefore, in these simulations were used:

$$T_E(E) = T_{E0}, \ T_I(I) = T_{I0} \text{ and } T_A(A) = T_{A0} \quad (4)$$
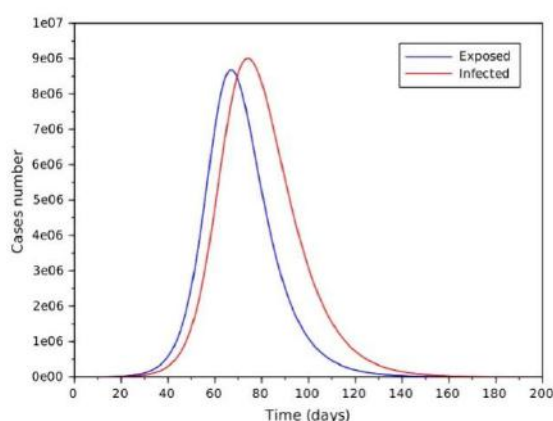

Fig. 6: Result of the numerical simulation for the size of the Coronavirus epidemic in the State of São Paulo using constant transmission rates.

However, it is still necessary to find the values of the rate(θ_1)and the environment-to-human constant transmission rate (T_{A0}) estimated by adjusting the data. In this case, we used the same set of data provided in Table 1 and we found the following values:$\theta_1 \cong 4.026$ and$T_{A0} \cong 6,39x10^{-10}$, with a normalized mean square error of 0,0327.

Figure 6 shows a prediction of epidemic size in the State of São Paulo considering rates constant of transmission. Comparing Figure 6 to Figure 2, the higher existence of infected individuals is clearly observed; mainly the value found for the peak of the infection which is around $9x10^6$ infected people which is an extremely high value and notoriously unrealistic. This result, obtained in the computer simulations, proves that the use of constant transmission rates can overestimate the severity of the Coronavirusepidemic and generate misleading information, because when using constant transmission rates, the control measures that are ongoing in the State of São Paulo are not taken into account.

IV.   DISCUSSION

In this study we use computational mathematical modeling to research the Coronavirus epidemic that is underway in the State of São Paulo – Brazil, and we carried out a detailed analysis of the epidemic using publicly released data. We adopted a model to clarify the transmission dynamics of the new Coronavirus and we analyzed the impact caused by the interventions taken by the government of the State of São Paulo, to decrease the number of infected people. The model adopted in this study uses non-constant transmission rates that change with the epidemiological status and with the conditions of the environment, reflecting the impact of the control measures implemented in the State. Another characteristic of this model is the incorporation of a new differential equation that represents the environmental contribution to the dynamics of disease transmission.

Through numerical simulation, an estimate was obtained for the basic reproduction number, $\mathfrak{R}_0 = 3.0745$, which consists of three parts and represents different transmission routes, namely, the route of exposed individuals, the route of the infected individuals and the route from the environmental reservoir to susceptible individuals. In particular, we observed that the contribution of the environmental reservoir, measured by$\mathfrak{R}_3$, is significant for the overall risk of the disease.

It is worth mentioning that through numerical simulation, a very satisfactory predictions of confirmed

cases of infected individuals was obtained from the 24th of March to the 24th of April 2020. In this simulation, we anticipate the appearance of an epidemic peak that will occur around 2 June 2020 with approximately39,000 infected individuals, after which the level of infection will decrease and approach an endemic state in the long term. Our study has important practical implications for those responsible for public health. The high level of reproduction of the Coronavirus suggests that the outbreak may be more serious than reported to date, given the growing social contacts and the breakdown of social isolation and effective and rigorous health measures in some places in the state.

In this work, we also perform some numerical simulations using constant transmission rates. The results showed an excessively larger epidemic peak that does not match reality. These unrealistic results were caused by the fixed transmission rates that do not reproduce the result of the isolation and control measures of the infected people in progress in the State of São Paulo. We believe that the use of dependent rates can generate more practical and reliable results, resulting in an estimate close to the current reality of the epidemic of the new Coronavirus in the State of São Paulo.

Analyzing the results obtained in our mathematical modeling, in particular with our simulations computational, the results suggest that Coronavirus infection should be combated for a longer period than the current epidemic, in order to reduce the endemic burden and potentially eliminate the disease. Vaccines, which are currently under development, are other intervention strategies for the new Coronavirus.

Finally, we emphasize that our mathematical modeling was based on the confirmed cases of infected individuals for the State of São Paulo from March 24 to April 24, 2020. Therefore, our predictions regarding the duration and size of the new epidemic Coronavirus should be interpreted as applicable only to confirmed cases in the State of São Paulo, data reported daily by the Ministry of Health. Problems regarding the accuracy, standard and reliability of confirmed cases of infected individuals are beyond the scope of this study.

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